

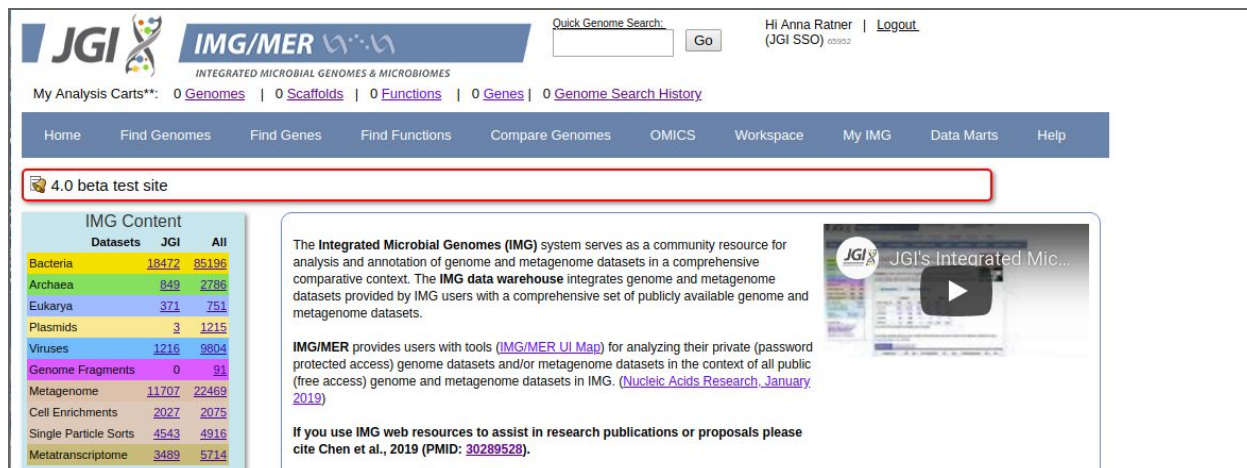
# Metagenome Bins

## Introduction

Metagenome bins can be accessed in IMG in a variety of ways:

### 1. Access via Table of Metagenomes

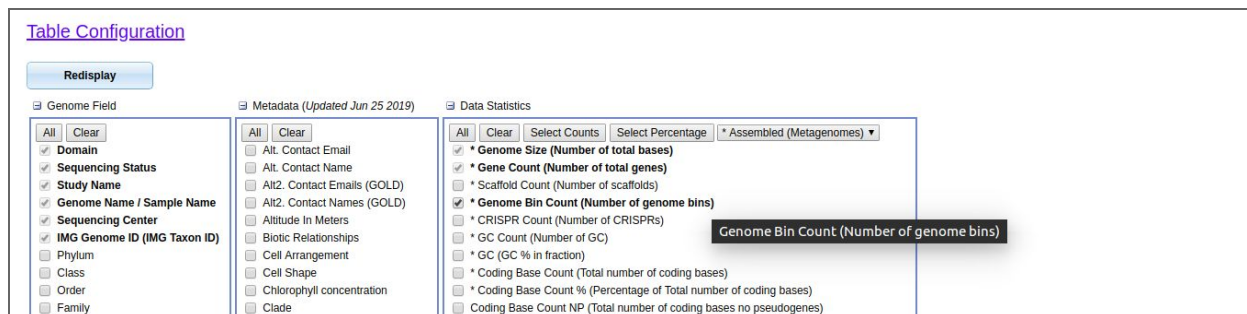
One way to access bins is directly from a table of metagenomes e.g. by clicking on the count of JGI Metagenomes on the IMG home page under IMG Content.



The screenshot shows the JGI IMG/MER homepage. The 'IMG Content' table is visible, showing counts for various datasets. The 'Genome Bin Count' is highlighted in the table configuration section.

Dataset	JGI	All
Bacteria	18472	85196
Archaea	849	2786
Eukarya	371	751
Plasmids	3	1215
Viruses	1216	9804
Genome Fragments	0	91
Metagenome	11707	22469
Cell Enrichments	2027	2075
Single Particle Sorts	4543	4916
Metatranscriptome	3489	5714

When the table of metagenomes comes up, the user needs to select “**Genome Bin Count**” from the Table Configuration option below the table and click “Redisplay”.



The screenshot shows the 'Table Configuration' dialog box. The 'Genome Bin Count' option is selected under the 'Data Statistics' tab.

**Table Configuration**

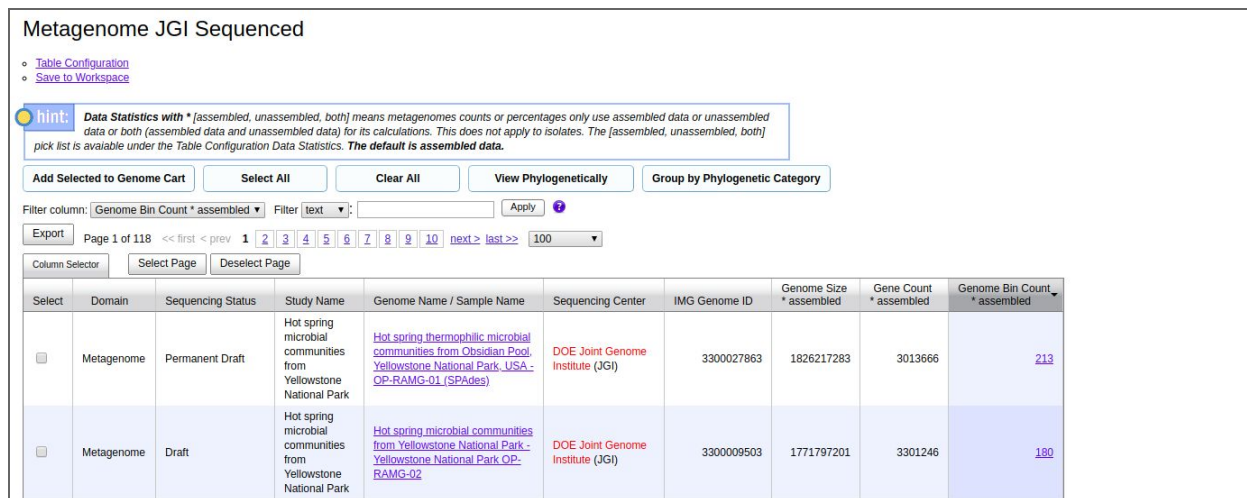
Redisplay

Genome Field: All, Clear, Domain, Sequencing Status, Study Name, Genome Name / Sample Name, Sequencing Center, IMG Genome ID (IMG Taxon ID), Phylum, Class, Order, Family.

Metadata (Updated Jun 25 2019): All, Clear, Alt. Contact Email, Alt. Contact Name, Alt2. Contact Emails (GOLD), Alt2. Contact Names (GOLD), Altitude In Meters, Biotic Relationships, Cell Arrangement, Cell Shape, Chlorophyll concentration, Clade.

Data Statistics: All, Clear, Select Counts, Select Percentage, \* Assembled (Metagenomes). \* Genome Size (Number of total bases), \* Gene Count (Number of total genes), \* Scaffold Count (Number of scaffolds), \* Genome Bin Count (Number of genome bins), \* CRISPR Count (Number of CRISPRs), \* GC Count (Number of GC), \* GC (GC % in fraction), \* Coding Base Count (Total number of coding bases), \* Coding Base Count % (Percentage of Total number of coding bases), \* Coding Base Count NP (Total number of coding bases no pseudogenes).

The table will then show the count of bins for each metagenome.



The screenshot shows the 'Metagenome JGI Sequenced' table. The table has columns for Domain, Sequencing Status, Study Name, Genome Name / Sample Name, Sequencing Center, IMG Genome ID, Genome Size, Gene Count, and Genome Bin Count.

Metagenome JGI Sequenced

Table Configuration, Save to Workspace

hint: Data Statistics with \* [assembled, unassembled, both] means metagenomes counts or percentages only use assembled data or unassembled data or both (assembled data and unassembled data) for its calculations. This does not apply to isolates. The [assembled, unassembled, both] pick list is available under the Table Configuration Data Statistics. The default is assembled data.

Add Selected to Genome Cart, Select All, Clear All, View Phylogenetically, Group by Phylogenetic Category

Filter column: Genome Bin Count \* assembled, Filter text, Apply

Export, Page 1 of 118, << first, prev, 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, next, last >>, 100

Select	Domain	Sequencing Status	Study Name	Genome Name / Sample Name	Sequencing Center	IMG Genome ID	Genome Size * assembled	Gene Count * assembled	Genome Bin Count * assembled
<input type="checkbox"/>	Metagenome	Permanent Draft	Hot spring microbial communities from Yellowstone National Park	Hot spring thermophilic microbial communities from Obsidian Pool, Yellowstone National Park, USA - OP-RAMG-01 (SPAdes)	DOE Joint Genome Institute (JGI)	3300027863	1826217283	3013666	213
<input type="checkbox"/>	Metagenome	Draft	Hot spring microbial communities from Yellowstone National Park	Hot spring microbial communities from Yellowstone National Park - Yellowstone National Park OP-RAMG-02	DOE Joint Genome Institute (JGI)	3300009503	1771797201	3301246	180

The bin count links to [bin detail page](#) with links to scaffolds and genes for each metagenome bin.

**Metagenome Bins**

Genome: [Hot spring thermophilic microbial communities from Obsidian Pool, Yellowstone National Park, USA - OP-RAMG-01 \(SPAdes\)](#)

[Save Selected Bins as Scaffold Sets](#)
[Select All](#)
[Clear All](#)

Filter column: [Bin ID](#) Filter [text](#) [Apply](#) [?](#)

[Export](#)
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[Column Selector](#)
[Select Page](#)
[Deselect Page](#)

Select	Bin ID	Bin Quality	Bin Lineage	Bin Completeness	Bin Contamination	Total Number of Bases	5s rRNA	16s rRNA	23s rRNA	tRNA Genes	Gene Count	Scaffold Count
<input type="checkbox"/>	<a href="#">3300027863_100</a>	MQ	Bacteria	75.59	0.54	2333895	0	0	0	<a href="#">33</a>	<a href="#">2294</a>	<a href="#">361</a>
<input type="checkbox"/>	<a href="#">3300027863_101</a>	MQ	Bacteria	89.45	0.18	2321820	<a href="#">1</a>	<a href="#">1</a>	0	<a href="#">45</a>	<a href="#">2119</a>	<a href="#">117</a>
<input type="checkbox"/>	<a href="#">3300027863_102</a>	HQ	Bacteria	92.74	4.95	2286351	<a href="#">1</a>	<a href="#">1</a>	<a href="#">1</a>	<a href="#">44</a>	<a href="#">2208</a>	<a href="#">112</a>
<input type="checkbox"/>	<a href="#">3300027863_103</a>	MQ	Bacteria	83.62	3.45	2275490	<a href="#">1</a>	0	<a href="#">1</a>	<a href="#">38</a>	<a href="#">2269</a>	<a href="#">288</a>
<input type="checkbox"/>	<a href="#">3300027863_104</a>	MQ	Bacteria	50.09	7.14	2263522	0	0	0	<a href="#">25</a>	<a href="#">2333</a>	<a href="#">456</a>
<input type="checkbox"/>	<a href="#">3300027863_105</a>	HQ	Bacteria	90.74	0	2266204	<a href="#">1</a>	<a href="#">2</a>	<a href="#">1</a>	<a href="#">44</a>	<a href="#">2164</a>	<a href="#">226</a>
<input type="checkbox"/>	<a href="#">3300027863_107</a>	MQ	Bacteria	97.63	0	2249348	<a href="#">2</a>	0	0	<a href="#">34</a>	<a href="#">2183</a>	<a href="#">172</a>
<input type="checkbox"/>	<a href="#">3300027863_108</a>	MQ	Bacteria ; Actinobacteria	95.44	1.28	2235363	<a href="#">1</a>	0	<a href="#">1</a>	<a href="#">45</a>	<a href="#">1922</a>	<a href="#">55</a>
<input type="checkbox"/>	<a href="#">3300027863_11</a>	HQ	Bacteria	92.59	1.75	5171146	<a href="#">3</a>	<a href="#">1</a>	<a href="#">2</a>	<a href="#">64</a>	<a href="#">4599</a>	<a href="#">211</a>
<input type="checkbox"/>	<a href="#">3300027863_110</a>	MQ	Bacteria	60.34	0	2240746	0	<a href="#">1</a>	<a href="#">1</a>	<a href="#">38</a>	<a href="#">2197</a>	<a href="#">156</a>
<input type="checkbox"/>	<a href="#">3300027863_112</a>	MQ	Bacteria	89.41	5.91	2213099	<a href="#">1</a>	<a href="#">1</a>	0	<a href="#">42</a>	<a href="#">2183</a>	<a href="#">202</a>
<input type="checkbox"/>	<a href="#">3300027863_113</a>	MQ	Bacteria	78.85	7.79	2193531	0	0	<a href="#">1</a>	<a href="#">32</a>	<a href="#">2047</a>	<a href="#">316</a>

## 2. Access via Metagenome Detail Page

If the user is interested in a particular metagenome which has bins, the bins can be accessed directly from the metagenome details page.

**Microbiome Details (Assembled Data)**

[Add to Genome Cart](#)
[Browse Genome](#)
[BLAST Genome](#)
[Download Data](#)

**About Genome**

- [Overview](#)
- [Statistics](#)
- [Genes](#)

**Overview**

<b>Study Name (Proposal Name)</b>	Freshwater sediment methanotrophic microbial communities from Lake Washington under simulated oxygen tension
<b>Sample Name</b>	Freshwater sediment methanotrophic microbial communities from Lake Washington under simulated oxygen tension - Sediment Metagenome 20_HOW5 (SPAdes)
<b>Taxon Object ID</b>	3300024970
<b>IMG Submission ID</b>	<a href="#">183866</a>
<b>GOLD ID in IMG Database</b>	
<b>GOLD Analysis Project Id</b>	<a href="#">Ga0207967</a>
<b>GOLD Analysis Project Type</b>	Metagenome Analysis
<b>Submission Type</b>	Reanalysis
<b>JGI Analysis Product Name</b>	Metagenome Minimal Draft
<b>JGI Analysis Project Type</b>	Metagenome Analysis
<b>Sequencing Status</b>	Draft
<b>Sequencing Center</b>	DOE Joint Genome Institute (JGI)
<b>IMG Release/Pipeline Version</b>	IMG Annotation Pipeline v.4.16.2

CRISPR Count	125	-
<b>Genes</b>		
RNA genes	1115	0.69%
rRNA genes	189	0.12%
5S rRNA	48	0.03%
16S rRNA	55	0.03%
18S rRNA	6	0.00%
23S rRNA	76	0.05%
28S rRNA	4	0.00%
tRNA genes	926	0.57%
Protein coding genes	161581	99.31%
with Product Name	113715	69.89%
with COG	100026	61.48%
with Pfam	97812	60.12%
with KO	80968	49.77%
with Enzyme	43842	26.95%
with MetaCyc	26180	16.09%
with KEGG	46017	28.28%
COG Clusters	3350	72.34%
Pfam Clusters	4591	28.16%
Metagenome Bins	4	

### 3. Access via Overview of Bins

Metagenome Bins can be accessed in a more efficient manner from the “Find Genomes” menu. They can be viewed in bulk either by Taxonomy or by Ecosystem. Both views present an overview of \*all\* bins in IMG in a **partition viewer**.

The horizontal partition layout is a way to represent a tree hierarchy where each node is drawn as a rectangle and its children are drawn as smaller adjacent rectangle branches. The height of all the child rectangles matches the height of the parent rectangle. The placement and height of each child node corresponds to the number of leaf nodes in its branch of the tree.

To navigate within the partition, the user can:

1. Click on a parent rectangle of interest to expand that category. The legend will then display a list of all the child nodes for that category, even those not visible in the viewer itself (this happens if the leaf count for the category is relatively low).
2. User can click on an item in the legend to expand that category.
3. User can click on any item in the breadcrumbs (displayed when hovering with the mouse over the partition) to see all items for that category in a bin details table.
4. User can click to the left of a category in the viewer to return to the parent category.

### Bins by Taxonomy

> [Home](#) > [Find Genomes](#) > [Bins by Taxonomy](#)

## Metagenome Bins by Taxonomy

Total Metagenomes with Bins: 7820  
Total Bins: 67592

View by Phylogenetic Category:

--- Select a Category --- ▼



**hint:** Partition: click on a category in the legend to expand hierarchy under that category (the legend appears when a category is selected). Click on any category in the partition display to expand that category. Click to the left of that category to return to the parent category. Click on a breadcrumb category (displayed when hovering with the mouse over the partition) to display the list of items for the hierarchy up to that category.



## Metagenome Bins by Taxonomy

Total Metagenomes with Bins: 7820  
Total Bins: 67592

View by Phylogenetic Category:

--- Select a Category --- ▼

--- Select a Category --- ▼

Reset

Domain

Phylum

Class

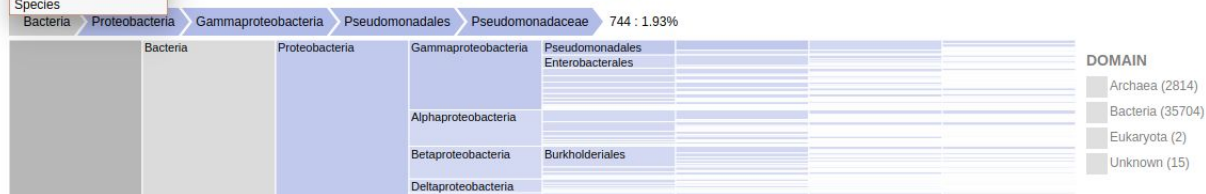
Order

Family

Genus

Species

Partition: click on a category in the legend to expand hierarchy under that category (the legend appears when a category is selected). Click on any category in the partition display to expand that category. Click to the left of that category to return to the parent category. Click on a breadcrumb category (displayed when hovering with the mouse over the partition) to display the list of items for the hierarchy up to that category.



Metagenome Bins can also be **viewed grouped in a table by a category** of choice. The user can select from a dropdown list of categories. This table displays the count of bins for each item in that category “hierarchy”. The count links to bin details for that category hierarchy. As noted in the tool, duplicate category names may appear in the table. These would have a distinct hierarchy for the corresponding bins.

## Metagenome Bins by Phylogenetic Category

View by Phylogenetic Category:

Phylum ▼



**hint:** Click on the count to view the bin details for selected category.  
To group bins by a different category, choose from the dropdown above.  
Select 'Reset' to go back to view all categories in the partition viewer.  
Note: Duplicate category names may appear. These would have a distinct hierarchy for the corresponding bins.

Show 10 ▼ entries

Search: therm x

Phylum ▲	Bin Count ▴
Coprothermobacterota	5
Deinococcus-Thermus	211
Rhodothermaeota	4
Thermodesulfobacteria	25
Thermotogae	188

Showing 1 to 5 of 5 entries (filtered from 66 total entries) Previous 1 Next

## Bins by Ecosystem

> Home > Find Genomes > Bins by Ecosystem

### Metagenome Bins by Ecosystem

Total Metagenomes with Bins: 7820

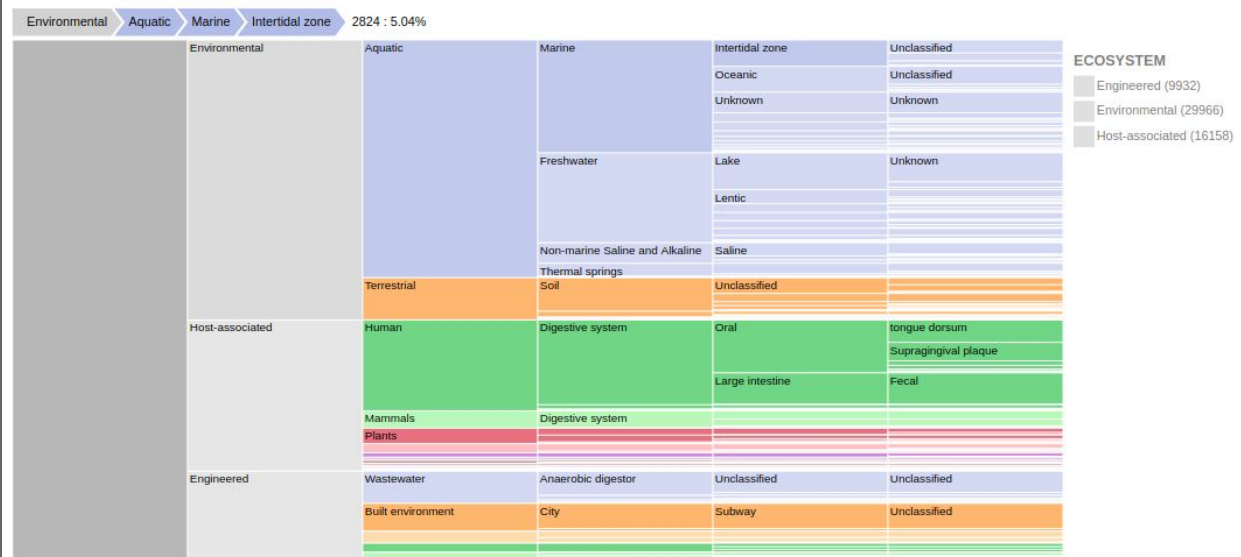
Total Bins: 67592

View by Ecosystem Category:

--- Select a Category --- ▼



**hint:** Partition: click on a category in the legend to expand hierarchy under that category (the legend appears when a category is selected). Click on any category in the partition display to expand that category. Click to the left of that category to return to the parent category. Click on a breadcrumb category (displayed when hovering with the mouse over the partition) to display the list of items for the hierarchy up to that category.





## Metagenome Bins by Ecosystem

Total Metagenomes with Bins: 7820  
Total Bins: 67592

View by Ecosystem Category:

--- Select a Category ---

--- Select a Category ---

Reset

Ecosystem

Ecosystem Category

Ecosystem Type

Ecosystem Subtype

Specific Ecosystem

Click on a category in the legend to expand hierarchy under that category (the ; when a category is selected). Click on any category in the partition display to link to the left of that category to return to the parent category. Click on a category played when hovering with the mouse over the partition) to display the list of to that category.

Environmental Aquatic 25432 : 45.4%



## Metagenome Bins by Ecosystem Category

View by Ecosystem Category:

Ecosystem Category

hint:

Click on the count to view the bin details for selected category.  
To group bins by a different category, choose from the dropdown above.  
Select 'Reset' to go back to view all categories in the partition viewer.  
Note: Duplicate category names may appear. These would have a distinct hierarchy for the corresponding bins.

Show 10 entries

Search:

Ecosystem_category	Bin Count
Air	23
Algae	323
Animal	451
Annelida	142
Aquatic	25432
Arthropoda	984
Bioreactor	1281
Bioremediation	137
Biotransformation	386
Birds	107

Showing 1 to 10 of 29 entries Previous 1 2 3 Next

## Bins Details Table

The details table for any group of bins lists the bin IDs and links to associated genome, genes, and scaffolds:

### Metagenome Bins by Ecosystem

Ecosystem: Host-associated  
Ecosystem Category: Annelida

Save Selected Bins as Scaffold Sets

Select All

Clear All

Filter column: Bin ID Filter text: Apply

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Column Selector Select Page Deselect Page

Select	Bin ID	Genome Name	Ecosystem	Ecosystem Type	Ecosystem Subtype	Specific Ecosystem	Bin Quality	Bin Lineage	Bin Completeness	Bin Contamination	Total Number of Bases	5s rRNA	16s rRNA	23s rRNA	tRNA Genes	Gene Count	Scaffold Count
<input type="checkbox"/>	2004178001_1	<a href="#">Olivinus algarvensis microbial communities from Capo di Saint Andrea bay, Elba, Italy; Delta</a>	Host-associated	Annelida	Integument	Unclassified	MQ	Bacteria ; Proteobacteria ; Deltaproteobacteria ; unclassified ; unclassified	87.63	3.23	12744768	1	1	1	45	11503	198
<input type="checkbox"/>	3300003129_2	<a href="#">Olivinus algarvensis microbial community from off the coast of Capo di Saint Andrea, Elba, Italy</a>	Host-associated	Annelida	Integument	Unclassified	MQ	Bacteria ; Proteobacteria	68.92	1.61	6131798	1	1	1	48	6484	602
<input type="checkbox"/>	3300003129_3	<a href="#">Olivinus algarvensis microbial community from off the coast of Capo di Saint Andrea, Elba, Italy</a>	Host-associated	Annelida	Integument	Unclassified	MQ	Bacteria ; Proteobacteria ; Gammaproteobacter	91.99	2.73	4029764	0	0	0	34	4350	239

The table of bin scaffolds lists the scaffold IDs for the selected bin and links to table of genes for the selected bin scaffold.

Metagenome Bin Scaffolds

Genome: [Olavius algarvensis microbial communities from Capo di Sant'Andrea bay, Elba, Italy - Delta1](#)  
Bin name: 2004178001\_1

Add Selected to Scaffold Cart

Toggle Selected

Select All

Clear All

Filter column: Scaffold Filter text Apply ?

Export Page 1 of 2 << first < prev 1 2 next > last >> 100

Column Selector

Select Page

Deselect Page

Select	Scaffold	Gene Count	Sequence Length (bp)	GC Content	Lineage	5s rRNA	16s rRNA	23s rRNA	tRNA Genes
<input type="checkbox"/>	<a href="#">gws2_d1_0004_16</a>	<a href="#">396</a>	<a href="#">407380</a>	0.49	Bacteria ; Proteobacteria ; Deltaproteobacteria ; unclassified ; unclassified ; unclassified ; Olavius algarvensis sulfate-reducing endosymbiont	0	0	0	<a href="#">1</a>
<input type="checkbox"/>	<a href="#">gws2_d1_0005_2</a>	<a href="#">382</a>	<a href="#">359424</a>	0.49	Bacteria ; Proteobacteria	0	0	0	<a href="#">2</a>
<input type="checkbox"/>	<a href="#">gws2_d1_0006_16</a>	<a href="#">270</a>	<a href="#">312075</a>	0.51	Bacteria ; Proteobacteria ; Deltaproteobacteria ; unclassified ; unclassified ; unclassified	0	0	0	<a href="#">1</a>
<input type="checkbox"/>	<a href="#">gws2_d1_0007_7</a>	<a href="#">255</a>	<a href="#">267432</a>	0.49	Bacteria	0	0	0	<a href="#">1</a>
<input type="checkbox"/>	<a href="#">gws2_d1_0008_4</a>	<a href="#">250</a>	<a href="#">265094</a>	0.50	Bacteria ; Proteobacteria ; Deltaproteobacteria ; unclassified ; unclassified ; unclassified	0	0	0	0

Metagenome Bin rRNA\_5S Genes in Scaffolds

Genome: [Olavius algarvensis microbial communities from Capo di Sant'Andrea bay, Elba, Italy - Delta1](#)  
Bin name: 2004178001\_1

Filter column: Gene ID Filter text Apply ?

Export Page 1 of 1 << first < prev 1 next > last >> All

Column Selector

Select Page

Deselect Page

Select	Gene ID	Locus Type	Locus Tag	Gene Product Name	Start Coord	End Coord	Strand	Scaffold
<input type="checkbox"/>	<a href="#">rRNA_1</a>	rRNA	rRNA_1	5S rRNA	206776	206896	-	<a href="#">gws2_d1_0013_13</a>

Export Page 1 of 1 << first < prev 1 next > last >> All

Add Selected to Gene Cart

Select All

Clear All